

Sequence Listings:

Applicant: Garvan Institute of Medical Research

Title of Invention: NPY-Y7 Receptor Gene

Prior Application Number: PP 4385

Prior Application Filing Date: 1998-06-29

Number of SEQ ID NOs: 5

Software: PatentIn Ver. 2.1

SEQ ID NO: 1 Length: 14 Type: PRT

Organism: Artificial Sequence

Feature:

Other Information: Description of Artificial Sequence: N-terminal

consensus sequence

Sequence: 1

Met Xaa Xaa Met Xaa Glu Lys Trp Asp Xaa Asn Ser Ser Glu

1 5 10

SEQ ID NO: Length: 408 Type: PRT

Organism: Homo sapiens

Sequence: 2

Met Phe Ile Met Asn Glu Lys Trp Asp Thr Asn Ser Ser Glu Asn Trp

1 5 10

His Pro Ile Trp Asn Val Asn Asp Thr Lys His His Leu Tyr Ser Asp

20 25 30

Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala

35 40 45

Ala Ile Phe Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met



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	50)				55	,				60				
Gly	Asn	Thr	. Val	. Val	Cys	Phe	lle	Val	Met	Ara	Asn	Lvs	His	Met	Hic
65					70					75		-1-		1100	80
Thr	Val	Thr	Asn			Ile	Leu	Asn			Ile	Ser	Asp	Leu	
Val	C1	T1 -	D1	85					90					95	
val	сту	TIE			Met	Pro	Ile			Leu	Asp	Asn	Ile	Ile	Ala
C1	m	ъ.	100					105					110		
сту	Trp			GIY	Asn	Thr	Met	Суѕ	Lys	Ile	Ser	Gly	Leu	Val	Gln
63	- 1	115					120					125			
стА	TTE	Ser	Val	Ala	Ala	Ser	Val	Phe	Thr	Leu	Val	Ala	Ile	Ala	Val
_	130					135					140				
Asp	Arg	Phe	Gln	Cys	Val	Val	Tyr	Pro	Phe	Lys	Pro	Lys	Leu	Thr	Ile
145					150					155					160
Lys	Thr	Ala	Phe	Val	Ile	Ile	Met	Ile	Ile	Trp	Val	Leu	Ala	Ile	Thr
				165					170					175	
Ile	Met	Ser	Pro	Ser	Ala	Val	Met	Leu	His	Val	Gln	Glu	Glu	Lys	Tyr
			180					185					190		
Tyr	Arg	Val	Arg	Leu	Asn	Ser	Gln	Asn	Lys	Thr	Ser	Pro	Val	Tyr	Trp
		195					200					205		_	-
Cys	Arg	Glu	Asp	Trp	Pro	Asn	Gln	Glu	Met	Arg	Lys	Ile	Tyr	Thr	Thr
	210					215					220		_		
Val	Leu	Phe	Ala	Asn	Ile	Tyr	Leu	Ala	Pro	Leu	Ser	Leu	Ile	Val	Ile
225					230					235					240
Met	Tyr	Gly	Arg	Ile	Gly	Ile	Ser	Leu	Phe	Arg	Ala	Ala	Val	Pro	
				245					250					255	
Thr	Gly	Arg	Lys	Asn	Gln	Glu	Gln	Trp	His	Val	Val	Ser	Arg	Lys	Lvs
			260					265					270	-	4
Gln	Lys	Ile	Ile	Lys	Met	Leu	Leu	Ile	Val	Ala	Leu	Leu	Phe	Ile	Leu
		275					280					285			
Ser	Trp	Leu	Pro	Leu	Trp	Thr	Leu	Met	Met	Leu	Ser	Asp	Tvr	Ala	Asp
	290					295					300	•	3 -	+-	[
Leu	Ser	Pro	Asn	Glu	Leu	Gln	Ile	Ile	Asn	Ile	Tyr	Ile	Tvr	Pro	Phe
305					310					315	-				320
Ala	His	Trp	Leu	Ala	Phe	Gly	Asn	Ser	Ser		Asn	Pro	Ile	Ile	
				325					330					335	-1-
Gly	Phe	Phe	Asn	Glu	Asn	Phe	Arg	Arg	Gly	Phe	Gln	Glu	Ala	Phe	Gln
			340				-	345	-				350		~~11
Leu	Gln	Leu	Cys	Gln	Lys	Arg	Ala		Pro	Met	Glu	Ala		ጥb r	T.e.v
		355				-	360	_		_		365	- <u>, -</u>	- ***	Jeu
												555			



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SEQ ID NO: 3 Length: 405 Type: PRT

Organism: Mus musculus

Sequence: 3

Met Ser Thr Met Ser Glu Lys Trp Asp Ser Asn Ser Ser Glu Ser Trp Asn His Ile Trp Ser Gly Asn Asp Thr Gln His His Trp Tyr Ser Asp 20 25 Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala 35 40 Ala Val Phe Ile Ser Ser Tyr Leu Leu Ile Phe Val Leu Cys Met Val Gly Asn Thr Val Val Cys Phe Ile Val Ile Arg Asn Arg His Met His 65 70 75 Thr Val Thr Asn Phe Leu Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu 90 Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala 100 105 Gly Trp Pro Phe Gly Ser Ser Met Cys Lys Ile Ser Gly Leu Val Gln 120 Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val 140 Asp Arg Phe Arg Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Val 150 155 Lys Thr Ala Phe Val Thr Ile Val Ile Ile Trp Gly Leu Ala Ile Ala 165 170 175 Ile Met Thr Pro Ser Ala Ile Met Leu His Val Gln Glu Glu Lys Tyr 185 Tyr Arg Val Arg Leu Ser Ser His Asn Lys Thr Ser Thr Val Tyr Trp

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		195					200					205			
Cys	Arg	Glu	Asp	Trp	Pro	Arg	His	Glu	Met	Arg	Arg		Tyr	Thr	Thr
	210					215					220		_		
Val	Leu	Phe	Ala	Ile	Ile	Tyr	Leu	Ala	Pro	Leu	Ser	Leu	Ile	Val	Ile
, 225					230					235					240
Met	Tyr	Ala	Arg	Ile	Gly	Ala	Ser	Leu	Phe	Lys	Thr	Ala	Ala	His	Cys
				245					250					255	-
Thr	Gly	Lys	Gln	Arg	Pro	Val	Gln	Cys	Met	Tyr	Gln	Glu	Lys	Gln	Lys
			260					265					270		
Val	Ile	Lys	Met	Leu	Leu	Thr	Val	Ala	Leu	Leu	Phe	Ile	Leu	Ser	Trp
		275					280					285			
Leu	Pro	Leu	Trp	Thr	Leu	Met	Met	Leu	Ser	Asp	Tyr	Thr	Asp	Leu	Ser
	290					295					300				
	Asn	Lys	Leu	Arg	Ile	Ile	Asn	Ile	Tyr	Ile	Tyr	Pro	Phe	Ala	His
305					310					315					320
Trp	Leu	Ala	Phe	Cys	Asn	Ser	Ser	Val	Asn	Pro	Ile	Ile	Tyr	Gly	Phe
				325					330					335	
Phe	Asn	Glu	Asn	Phe	Arg	Asn	Gly	Phe	Gln	Asp	Ala	Phe	Gln	Ile	Cys
			340					345					350		
Gln	Lys	Lys	Ala	Lys	Pro	Gln	Glu	Ala	Tyr	Ser	Leu	Arg	Ala	īуs	Arg
_		355					360					365			
Asn	Ile	Val	Ile	Asn	Thr		Gly	Leu	Leu	Val	Gln	Glu	Pro	Val	Ser
61	370	_				375					380				
GIN	Asn	Pro	Gly	Gly		Asn	Leu	Gly	Cys	Gly	Lys	Ser	Ala	Asp	Asn
385	***	_	_	_	390					395					400
Pro	His	Arg	Asn												
				405											

SEQ ID NO: 4 Length: 1903 Type: DNA

Organism: Homo sapiens

Sequence: 4

ctcgagatcc attgtgctct aaaggcctcc tgagtagctg ggactacagg cgcccgccac 60 cacgcctggc taatttttt gtatttag tagggacggc gtttcactgt gttagccaga 120 tggtctccat ctccgacct cgtgatccac ccacctcggc ctcccaaagt gctgggatta 180



caggcgtgag	accgcgcccg	gccaatttcc	tttcttagtt	gcctctgccc	acctcttctc	240
				ggatgttaat		
				gagtgaagca		
				ctcttcagaa		
				agatattaat		
				cattatttcc		
				tattgtaatg		
				cataagtgat		
				agcaggatgg		
				tgtcgcagct		
				ctaccctttt		
				ggtcctagcc		
				atattaccga		
				agactggcca		
				cctggctccc		
				ggctgcagtt		
				gaagcagaag		
				gcccctgtgg		
				gatcatcaac		
				caatcccatc		
				ccagctccag		
				aagccatgtg		
				tcatggggaa		
				gaagaattaa		
				taactctact		
				ttttcaaaga		
				aaataaacaa		
				gtgacttaga		1860
		gaacagttaa				1903

SEQ ID NO: 5 Length: 1228 Type: DNA

Organism: Mus musculus

Sequence:

1228

ccacacagga atccttgata gaggaatg



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atgtecaeca igagegagaa atgggaetea aactetteag aaagetggaa teacatetgg 60 agtggcaatg atacacagca tcactggtat tcagatatca acattaccta tgtgaactac 120 tatctccacc agccccaagt ggcagctgtc ttcatcagct cctacctcct gatctttgtc 180 ttgtgcatgg tgggaaatac tgtcgtttgc tttattgtga taaggaatag acacatgcac 240 acagtcacta atttcttgat cttaaacctt gccataagtg atttactggt tggaatattc 300 tgtatgccta tcacattgct ggacaacatc atagcaggat ggccattcgg aagcagcatg 360 tgcaagatca gtgggctggt gcaagggata tcagttgcgg cttccgtctt caccttggtt 420 gcaatagctg tggacagatt ccgctgtgtg gtctacccct ttaagccaaa gctcactgtc 480 aagacageet ttgtcaegat tgtgateate tggggeetgg ceategeeat tatgaeteea 540 tetgeaataa tgttacatgt acaagaagaa aaatactace gtgtgagaet cageteecae 600 aataaaacca gcacagtcta ctggtgtcgg gaggactggc caagacacga aatgaggagg 660 atctatacca eggtgetatt tgccatcate tatettgete eteteteaet cattgttate 720 atgtatgcaa ggattggggc ttccctcttc aagacggcag cacactgcac aggcaagcag 780 cgtccagtgc agtgcatgta tcaagagaaa cagaaggtca tcaagatgct gctgactgtg 840 gccctccttt tcatcctttc ctggcttccc ctgtggaccc tgatgatgct ctcagactat 900 actgacctgt ctcctaacaa actgcgtatc atcaacatct acatctaccc tttcgcccac 960 tggctcgcct tctgcaacag cagtgtcaac cctattattt atggattctt taatgaaaat 1020 tttcgcaatg gtttccaaga tgctttccag atctgccaaa agaaagccaa gccccaggaa 1080 gectattece tgagagegaa aegeaacata gteataaaca eategggeet getggtgeag 1140 gaaccggtgt ctcaaaaccc aggtggggaa aatttgggat gtggaaaaag tgcagacaat 1200